



OIEP

RAW SEQUENCE LISTING

DATE: 02/12/2002

PATENT APPLICATION: US/09/942,429A

TIME: 10:51:33

Input Set : A:\W122217.txt

Output Set: N:\CRF3\02122002\I942429A.raw

3 <110> APPLICANT: JORGE H. CAPDEVILA, MICHAEL WATERMAN, AND VIJAKUMAR HOLLA
 5 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO
 6 HYPERTENSION
 8 <130> FILE REFERENCE: 22000.0110U2
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/942,429A
 C--> 10 <141> CURRENT FILING DATE: 2000-08-29
 10 <150> PRIOR APPLICATION NUMBER: 60/228,947
 11 <151> PRIOR FILING DATE: 2000-08-29
 13 <160> NUMBER OF SEQ ID NOS: 9
 15 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 4123
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Artificial Sequence
 22 <220> FEATURE:
 23 <223> OTHER INFORMATION: Description of Artificial Sequence; Note =
 24 synthetic construct
 26 <221> NAME/KEY: misc_feature
 27 <222> LOCATION: (1)...(4123)
 28 <223> OTHER INFORMATION: n = g, a, c or t(u)
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 32 cctgtcccaa gaaatggact ggatctttca atcatttact catccaacaa atatttgaag 120
 33 ttgtaaaatg accacaaagt gggctaaaag ttcagacgta tggagcatgt ccctctcggt 180
 34 ctttggtttt gaccaaagct cagaattgtg gaaagaaaga aaaagtagtg ggttatgcat 240
 35 gttgtgtcac agtgggaagt gaagtagtgg gtgttaaaga aaatgtttgg atagataaag 300
 36 gatcaagtga gcggcaacaa cacattcctg gcagagtga tgggctggct ttctagagat 360
 37 tcttggttaa ataccttttg tgtttgcctc tttgtggtct tcacaactag gattaattta 420
 38 gggaagataa tcatgatcca ggtgaggata aagattccag agaaaggctt atttctaccc 480
 39 cttaacttct ttgtttttct tcctttctaa aagttttgtc atttttataa tttatttttt 540
 40 atttaatttt ttcatgcaa tataatttga tcatattctt tccttcctcc aacttctcct 600
 41 agatcctcag ggccttccta gctatccatc tcatgttaa tggatagact gacaaccaa 660
 42 acattctttc tctgcttaaa taatatctcc ataaaatcta taaataaatg aggtagtgg 720
 43 aaactatctc agcacttttc aattgattgg ctagtaatcc ttcaatatct catttttttt 780
 44 aactttcgct ttatctattc tgtgtgnaca ttaatttttt tcaggcaagg cataatatat 840
 45 atataattgg actgatttct ttattagagt ttgccctatg tgagggtcaag aaatattctt 900
 46 aaattaatga gtgactgaat aagtgatggg caatttaagt atttagaaaa gaaagggttt 960
 47 attattccat tcagtcaaga tagtgagaca gagaaagagt ctgtcacagg ctgtgtatgt 1020
 48 ggtgaggctg attgagtctt gagccacctg aatgcaactg cactgttcca cctgctggca 1080
 49 catccatcct ggatcaatct ggagtgtgac tgtgacaagt ctgagataaa atggaagaaa 1140
 50 cagctggatt tggagtccag atgcaaagat gactataggt agaaactttc agcaattaca 1200
 51 ttcatctgaa cacaccaact actgttgtca tcatttcacc ctgaaattag gaaaatagta 1260
 52 caagcagcta cacctattac atgttttgta aattagaatg tgaatttctt aatatccagg 1320

ENTERED

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53 ttaatgtcta gtccatgact ttacctcact agcaaggata tacataacat gcaatatgtg 1380
54 ctcaataaat agttgtgagt agttcagaga aatgggaatt ggtatacata tagatgttac 1440
55 caagactaga tactagagat ttgtttttac tgtttaccaa agctgatgtt gcagattaat 1500
56 aaactttgga ttctgaggtc agtctctgtc tgtcttctcc attccccctc ccacaagtag 1560
57 gtgtgtctac cttctcatga cttaaatgcg gttttctaaa catttagtga cactagtgtat 1620
58 ccagaaacta ctaaccatgg gttttttttt atttagccct acaaggtaact tggatgggat 1680
59 ctctgggttc ttccaatggg cttctttgct cagtctatatt ctgggtgctgt tcaaggcagt 1740
60 ccaattctac ttacgaaggc agtggctgct caagaccctc cagcatttcc catgcatgcc 1800
61 ttcccactgg ctttgggggc accatctgaa gggacaagga gctccagcag attcttatat 1860
62 gggtagagaa attcccaagt gcttgcctac agtgtctctc ggggagcaat atacgagtc 1920
63 tgctttatga tctgactat gtgaagggtg ttctggggag atcagatcca aaggcttctg 1980
64 gaatttatca attctttgct ccttgattg gttatggtt gctcctgttg aatgggaaga 2040
65 agtggttcca gcatcgggcg atgttgactc cagccttcca ctatgacatc ctcaaaccct 2100
66 atgtcaaaat catggcggac tctgtcaata taatgctaga taaatgggag aagcttgatg 2160
67 gccaggacca cctctggag atcttccact gtgtttcatt gatgacactg gacactgtta 2220
68 tgaagtgtgc ttccagctac caaggcagtg ttcagttgga tgaaaattcc aagttgtata 2280
69 ctaaggctgt cgaggatcta aacaacctga ctttctttcg cctgcggaat gccttttata 2340
70 agtacaacat catctacaat atgtcctctg atggacgttt gtcccaccat gcctgccaga 2400
71 ttgctcacga gcacacagat ggagtgtatc agatgaggaa gtctcagctg cagaatgagg 2460
72 aagagctgca gaaggccagg aagaagagac acttggattt cttggacatc ctcttgttg 2520
73 ccagaatgga ggataggaac agcttgtctg atgaggacct gcgtgcagag gtggacacat 2580
74 tcatgtttga gggcatgac actacagcca gtggaatttc ctggattttc tatgctctgg 2640
75 ccaccacccc tgagcaccaa cagagatgca gagaggaggt gcagagcatt ctgggtgatg 2700
76 gaacctctgt cacatgggac catctgggac agatgcccta caccaccatg tgcatcaagg 2760
77 aggccttgag gctctatcca ccagtaatat ctgtgagtcg agagctcagc tcacctgtca 2820
78 ccttcccaga tggacgtccc atacccaaag gtatcacagc cacaatttcc atttatggcc 2880
79 tacatcataa cccacgtttc tggccaaacc caaagggtgt tgacccctct agatttgcac 2940
80 cagattcttc tcaccatagc catgcttctc tgccattctc aggaggatca aggaactgca 3000
81 ttgggaaaca gtttgcctatg aacgagctga aggtggctgt ggcctgacc ctgcttctct 3060
82 ttgaattgct gccagatccc accaggatcc cagtcctcat tgcaagactt gtgttgaaagt 3120
83 ccaagaatgg gatccacctg tgtctcaaga agctaagata attctgatgg agtcagggca 3180
84 gctccagagg tctgtgcct gcaataacct cttttgtctc tggcttttct gtactttgct 3240
85 ttctctttga ttcccattct tctgtctctc gcaatgtgtc ctgtcatctc atctttctgc 3300
86 cctcatttct gtagcttttc ctctagacac ctctctaacc tgtgcatgta cctgtttccc 3360
87 atctcgtttt aactctgacc agccactgaa cctgcagcca gcagcctgtc cccagcctg 3420
88 ttcaccctc ataaccattg cactgacaga ggaagatata ttttagaggg agacacttgt 3480
89 acctttctct ccttcagtt attagactct tgggacaatg gacatcatga attaaaacgt 3540
90 tcttagaaat cacatgctgg gagaaaatta aactaaaat ctggtaccag ccagaggaag 3600
91 gaacttgact caaaataaga gatttttaga tatttctgtc tgtctcatag ttaaaattaa 3660
92 tgttttctct cttctggca tatgcctcat cttttctatg aagtagtaat actgatacag 3720
93 aaaggtagag agaaatgaat agtttttgct actttgggccc aaactgtgaa aaaatccatt 3780
94 ttatttctac aatttctgtt tccaatttcc atttaagaca caggaaaact actcagcatg 3840
95 aactttgggg agccagagca gttttggcaa tccagggaag catgttgcca tctggctcct 3900
96 actgttagaa tgtggtagaa ttctcagctc ctgagagggt gttctctgct tttgactcct 3960
97 gagctgggtg ttagaaatg caggttggcg tttttgtga agctaaggag ttttctgact 4020
98 ttaaccgggt cttatttgtt tagagtactc tgattattca ctttagtgat ttggagaatt 4080
99 cctattaaaa tcacatgaca tggaaaaaaa aaaaaaagg aat 4123

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101 <210> SEQ ID NO: 2

102 <211> LENGTH: 507

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103 <212> TYPE: PRT
104 <213> ORGANISM: Artificial Sequence
106 <220> FEATURE:
107 <223> OTHER INFORMATION: Description of Artificial Sequence; Note =
108     synthetic construct
110 <400> SEQUENCE: 2
111 Met Gly Phe Phe Val Phe Ser Pro Thr Arg Tyr Leu Asp Gly Ile Ser
112 1           5           10           15
113 Gly Phe Phe Gln Trp Ala Phe Leu Leu Ser Leu Phe Leu Val Leu Phe
114           20           25           30
115 Lys Ala Val Gln Phe Tyr Leu Arg Arg Gln Trp Leu Leu Lys Thr Leu
116           35           40           45
117 Gln His Phe Pro Cys Met Pro Ser His Trp Leu Trp Gly His His Leu
118           50           55           60
119 Lys Asp Lys Glu Leu Gln Gln Ile Leu Ile Trp Val Glu Lys Phe Pro
120 65           70           75           80
121 Ser Ala Cys Leu Gln Cys Leu Ser Gly Ser Asn Ile Arg Val Leu Leu
122           85           90           95
123 Tyr Asp Pro Asp Tyr Val Lys Val Val Leu Gly Arg Ser Asp Pro Lys
124           100          105          110
125 Ala Ser Gly Ile Tyr Gln Phe Phe Ala Pro Trp Ile Gly Tyr Gly Leu
126           115          120          125
127 Leu Leu Leu Asn Gly Lys Lys Trp Phe Gln His Arg Arg Met Leu Thr
128           130          135          140
129 Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Val Lys Ile Met Ala
130 145          150          155          160
131 Asp Ser Val Asn Ile Met Leu Asp Lys Trp Glu Lys Leu Asp Gly Gln
132           165          170          175
133 Asp His Pro Leu Glu Ile Phe His Cys Val Ser Leu Met Thr Leu Asp
134           180          185          190
135 Thr Val Met Lys Cys Ala Phe Ser Tyr Gln Gly Ser Val Gln Leu Asp
136           195          200          205
137 Glu Asn Ser Lys Leu Tyr Thr Lys Ala Val Glu Asp Leu Asn Asn Leu
138           210          215          220
139 Thr Phe Phe Arg Leu Arg Asn Ala Phe Tyr Lys Tyr Asn Ile Ile Tyr
140 225          230          235          240
141 Asn Met Ser Ser Asp Gly Arg Leu Ser His His Ala Cys Gln Ile Ala
142           245          250          255
143 His Glu His Thr Asp Gly Val Ile Lys Met Arg Lys Ser Gln Leu Gln
144           260          265          270
145 Asn Glu Glu Glu Leu Gln Lys Ala Arg Lys Lys Arg His Leu Asp Phe
146           275          280          285
147 Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asp Arg Asn Ser Leu Ser
148           290          295          300
149 Asp Glu Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly His
150 305          310          315          320
151 Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala Thr
152           325          330          335
153 His Pro Glu His Gln Gln Arg Cys Arg Glu Glu Val Gln Ser Ile Leu

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154          340          345          350
155 Gly Asp Gly Thr Ser Val Thr Trp Asp His Leu Gly Gln Met Pro Tyr
156          355          360          365
157 Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Leu Tyr Pro Pro Val Ile
158          370          375          380
159 Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly Arg
160 385          390          395          400
161 Ser Ile Pro Lys Gly Ile Thr Ala Thr Ile Ser Ile Tyr Gly Leu His
162          405          410          415
163 His Asn Pro Arg Phe Trp Pro Asn Pro Lys Val Phe Asp Pro Ser Arg
164          420          425          430
165 Phe Ala Pro Asp Ser Ser His His Ser His Ala Tyr Leu Pro Phe Ser
166          435          440          445
167 Gly Gly Ser Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu Leu
168          450          455          460
169 Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro Asp
170 465          470          475          480
171 Pro Thr Arg Ile Pro Val Pro Ile Ala Arg Leu Val Leu Lys Ser Lys
172          485          490          495
173 Asn Gly Ile His Leu Cys Leu Lys Lys Leu Arg
174          500          505
176 <210> SEQ ID NO: 3
177 <211> LENGTH: 508
178 <212> TYPE: PRT
179 <213> ORGANISM: Artificial Sequence
181 <220> FEATURE:
182 <223> OTHER INFORMATION: Description of Artificial Sequence; Note =
183     synthetic construct
185 <400> SEQUENCE: 3
186 Met Ser Ala Ser Ala Leu Ser Ser Ile Arg Phe Pro Gly Ser Ile Ser
187 1          5          10          15
188 Glu Tyr Leu Gln Val Ala Ser Val Leu Ser Leu Leu Leu Leu Leu Phe
189          20          25          30
190 Lys Thr Ala Gln Leu Tyr Leu His Arg Gln Trp Leu Leu Ser Ser Thr
191          35          40          45
192 Gln Gln Phe Pro Ser Pro Pro Ser His Trp Leu Phe Gly His Lys Ile
193          50          55          60
194 Leu Lys Asp Gln Asp Leu Gln Asp Ile Leu Thr Arg Ile Lys Asn Phe
195 65          70          75          80
196 Pro Ser Ala Cys Pro Gln Trp Leu Trp Gly Ser Lys Val Arg Ile Gln
197          85          90          95
198 Val Tyr Asp Pro Asp Tyr Met Lys Leu Ile Leu Gly Arg Ser Asp Pro
199          100          105          110
200 Lys Ala Asn Gly Ser Tyr Arg Phe Leu Ala Pro Trp Ile Gly Arg Gly
201          115          120          125
202 Leu Leu Met Leu Asp Gly Gln Thr Trp Phe Gln His Arg Arg Met Leu
203          130          135          140
204 Thr Pro Ala Phe His Tyr Asp Ile Leu Lys Pro Tyr Thr Glu Ile Met
205 145          150          155          160

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```

206 Ala Asp Ser Val Arg Val Met Leu Asp Lys Trp Glu Gln Ile Val Gly
207           165           170           175
208 Gln Asp Ser Thr Leu Glu Ile Phe Arg His Ile Thr Leu Met Thr Leu
209           180           185           190
210 Asp Thr Ile Met Lys Cys Ala Phe Ser His Glu Gly Ser Val Gln Leu
211           195           200           205
212 Asp Arg Lys Tyr Lys Ser Tyr Ile Gln Ala Val Glu Asp Leu Asn Asp
213           210           215           220
214 Leu Val Phe Ser Arg Val Arg Asn Ile Phe His Leu Asn Asp Ile Ile
215 225           230           235           240
216 Tyr Arg Val Ser Ser Asn Gly Cys Lys Ala Asn Ser Ala Cys Gln Leu
217           245           250           255
218 Ala His Asp His Thr Asp Gln Val Ile Lys Ser Arg Arg Ile Gln Leu
219           260           265           270
220 Gln Asp Glu Glu Glu Leu Glu Lys Leu Lys Lys Lys Arg Arg Leu Asp
221           275           280           285
222 Phe Leu Asp Ile Leu Leu Phe Ala Arg Met Glu Asn Gly Lys Ser Leu
223           290           295           300
224 Ser Asp Lys Asp Leu Arg Ala Glu Val Asp Thr Phe Met Phe Glu Gly
225 305           310           315           320
226 His Asp Thr Thr Ala Ser Gly Ile Ser Trp Ile Phe Tyr Ala Leu Ala
227           325           330           335
228 Thr Asn Pro Glu His Gln Gln Arg Cys Arg Lys Glu Ile Gln Ser Leu
229           340           345           350
230 Leu Gly Asp Gly Thr Ser Ile Thr Trp Asn Asp Leu Asp Lys Met Pro
231           355           360           365
232 Tyr Thr Thr Met Cys Ile Lys Glu Ala Leu Arg Ile Tyr Pro Pro Val
233           370           375           380
234 Pro Ser Val Ser Arg Glu Leu Ser Ser Pro Val Thr Phe Pro Asp Gly
235 385           390           395           400
236 Arg Ser Leu Pro Lys Gly Ile His Val Met Leu Ser Phe Tyr Gly Leu
237           405           410           415
238 His His Asn Pro Thr Val Trp Pro Asn Pro Glu Val Phe Asp Pro Ser
239           420           425           430
240 Arg Phe Ala Pro Gly Ser Ser Arg His Ser His Ser Phe Leu Pro Phe
241           435           440           445
242 Ser Gly Gly Ala Arg Asn Cys Ile Gly Lys Gln Phe Ala Met Asn Glu
243           450           455           460
244 Leu Lys Val Ala Val Ala Leu Thr Leu Leu Arg Phe Glu Leu Leu Pro
245 465           470           475           480
246 Asp Pro Thr Arg Val Pro Ile Pro Ile Pro Arg Ile Val Leu Lys Ser
247           485           490           495
248 Lys Asn Gly Ile His Leu His Leu Lys Glu Leu Gln
249           500           505
251 <210> SEQ ID NO: 4
252 <211> LENGTH: 2116
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\W122217.txt

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:564 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:566 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:568 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:569 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:570 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:571 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:573 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:576 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:577 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:578 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

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L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:591 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

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L:594 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:595 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

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L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:608 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

L:610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9

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L:611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:613 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9